An HRD/DER-independent ER quality control mechanism involves Rsp5p-dependent ubiquitination and ER-Golgi transport

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We have identified a new pathway of ER-associated degradation in Saccharomyces cerevisiae that functions separately from the HRD/DER pathway comprised of Hrd1p, Hrd3p, Der1p, and Ubc7p. This pathway, termed Hrd1p independent-proteolysis (HIP), is capable of recognizing and degrading both luminal (CPY* and PrA*) and integral membrane proteins (Sec61–2p) that misfold in the ER. CPY* overexpression likely saturates the HRD/DER pathway and activates the HIP pathway, so the slowed degradation kinetics of CPY* in a hrd1 Δ strain is restored to a wild-type rate when CPY* is overexpressed. Substrates of HIP require vesicular trafficking between the ER and Golgi apparatus before degradation by the ubiquitin-proteasome system. Ubiquitination of HIP substrates does not involve the HRD/DER pathway ubiquitin ligase Hrd1p, but instead uses another ubiquitin ligase, Rsp5p. HIP is regulated by the unfolded protein response as Ire1p is necessary for the degradation of CPY* when overexpressed, but not when CPY* is expressed at normal levels. Both the HIP and HRD/DER pathways contribute to the degradation of CPY*, and only by eliminating both is CPY* degradation completely blocked.

Introduction

The highly conserved eukaryotic secretory pathway initiates at the ER, where proteins enter through the Sec61p-mediated translocon in an unfolded state (Deshaies et al., 1991). In the lumen of the ER, proteins undergo folding and maturation involving glycosylation, disulfide bond formation, and oligomerization. Before exiting the ER, proteins must first pass an ER quality control (ERQC)* system that ensures correct folding and processing has transpired (Brodsky and McCracken, 1999; Ellgaard et al., 1999). Failure to pass this quality control checkpoint results in the protein’s degradation, preventing any toxic consequences that may result from an accumulation of aberrant proteins in the secretory pathway (Kopito, 1997; Plenmer and Wolf, 1999). Quality control within the secretory pathway involves ER retention, ER-associated degradation (ERAD) and potential retrieval from downstream organelles (Ellgaard et al., 1999). ERQC uses molecular chaperones (Brodsky et al., 1999) and glycosylation events (Hebert et al., 1995; Jakob et al., 1998) to recognize misfolded or unassembled proteins. Such proteins are exported from the ER to the cytosol via the translocon and are degraded. The most well-characterized facet of ERAD occurs in yeast and utilizes the HRD/DER pathway (Wilhovsky et al., 2000) or HRD complex (Gardner et al., 2000). The HRD/DER pathway consists of Hrd1p/Der3p, Hrd3p, Der1p, and the ubiquitin-conjugating enzymes Ubc7p and Ubc1p, which together act to deliver misfolded proteins to the proteasome (Hampton et al., 1996; Knop et al., 1996; Bordallo et al., 1998; Friedlander et al., 2000). Hrd1p/Der3p, an ER-integral membrane protein, is the E3-ubiquitin ligase whose cytosolically positionedRING-H2 domain mediates the specific covalent attachment of ubiquitin to the target substrates (Bays et al., 2001; Deak and Wolf, 2001). Hrd3p regulates Hrd1p (Gardner et al., 2000), whereas the function of Der1p remains unknown (Knop et al., 1996).

ERQC contributes to the manifestation of a number of diseases by either depleting cells of essential proteins, or by the accumulation and aggregation of misfolded/mutant proteins it is incapable of degrading. Such substrates include the following: CFTR-ΔF508 (Ward et al., 1995), α1-antitrypsin inhibitor (Teckman and Perlmuter, 1996), unassembled T cell receptor subunits (Bonifacino et al., 1989), and apoB under conditions of limited lipid availability (Fisher et al., 1997). Pathogens are able to promote or conceal their infection...
by manipulating the ERQC system to degrade CD4 or MHC class I heavy chain molecules (Margottini et al., 1996; Wiertz et al., 1996), whereas bacterial toxins usurp ERQC to access cytosolic targets (Simpson et al., 1999). ERQC substrates characterized in yeast include CPY* and PrA*, which are mutant forms of the yeast vacuolar carboxypeptidase Y (CPY) and proteinase A (PrA), respectively, that are retained in the ER (Knoop et al., 1996), and Sec61–2p, which is a mutant subunit of the translocon (Biederer et al., 1996). Finally, the ERQC-degradative machinery also acts in a regulatory role to moderate the half-life of correctly folded proteins such as HMG-CoA reductase in response to cellular signals so as to modulate the sterol-synthesizing mevalonate pathway (Hampton et al., 1996).

The ERQC is intimately associated with the unfolded protein response (UPR), a wide-ranging cellular response to transcriptionally up-regulate a number of distinct mechanisms to cope with the ER stress encountered when increased amounts of misfolded proteins accumulate in the ER (Friedlander et al., 2000). ER stress is thought to be sensed by Ire1p and the chaperone Kar2p, which transduce the UPR signal from the ER to the nucleus where in yeast almost 400 genes are transcriptionally up-regulated, including those encoding molecular chaperones, components of the HRD1/DER pathway, and machinery responsible for vesicular transport between the ER and Golgi apparatus (Travers et al., 2000).

The HRD1/DER pathway is able to target a number of ERQC substrates for proteasomal degradation, yet CPY* turnover, while impaired in HRD1/DER-deficient strains, still proceeds at a substantial rate (Hill and Cooper, 2000). This slowed, but not abolished, degradation in the absence of Hrd1p is also the case for a number of other substrates (Wilhovsky et al., 2000). Furthermore, the inactivation of the HRD1/DER pathway has no effect on the degradation of unassembled Vph1p (Hill and Cooper, 2000) and Fur4–430Np (Wilhovsky et al., 2000). This HRD1/DER-independent means of degradation prompted the prediction of an additional degradative pathway (Hill and Cooper, 2000), or at a minimum an additional ubiquitin ligase (Wilhovsky et al., 2000).

Our interest in such an alternative degradative pathway resulted in the discovery of the requirement of ER-Golgi transport for efficient degradation of ERQC substrates (Caldwell et al., 2001). Inactivation of Sec12p (required for vesicle to exit the ER) or Sec18p (vesicle fusion with a post-ER compartment) significantly slowed the degradative rate of CPY* as did the absence of Erv29p (Caldwell et al., 2001). Erv29p is localized to the ER and Golgi apparatus, contains an ER-retrieval sequence, and behaves as a cargo loading/transport receptor that acts to transport a subset of lumenal proteins including CPY and PrA from the ER to the Golgi apparatus via COPII-coated vesicles (Belden and Barlowe, 2001; Caldwell et al., 2001). The absence of Erv29p severely retards the ER-Golgi transport of such ligands, yet the secretory pathway remains functional with invertase and alkaline phosphatase displaying normal transport kinetics (Caldwell et al., 2001). It is likely that CPY* also requires Erv29p to enter such transport vesicles and therefore, the absence of Erv29p severely impairs the transport of CPY* from the ER to the Golgi apparatus. This work investigates the role of ER-Golgi trafficking plays in ERQC and resulted in the identification of an HRD1/DER-independent ERQC mechanism capable of recognizing both lumenal and integral membrane substrates in the yeast Saccharomyces cerevisiae. This separate degradative mechanism requires ER-Golgi transport as evidenced by the requirement of Erv29p and Sec12p. We were able to directly observe this novel degradative mechanism by overexpressing CPY* because under these conditions the HRD1/DER pathway appears saturated, causing CPY* degradation to be totally dependent on this novel mechanism. Substrates targeted for degradation through this mechanism are ubiquitinated, even in the absence of Hrd1p, by the ubiquitin ligase Rsp5p. Only by removing both ERQC pathways is CPY* degradation completely blocked. Our data call attention to the complexity of quality control in the ER and show that mechanisms in addition to the HRD1/DER pathway are able to deliver misfolded proteins to the proteasome for degradation.

Results
CPY* degradation continues in HRD1/DER-deficient cells and requires ER-Golgi transport

The ERQC machinery is responsible for the ERAD of misfolded proteins and unassembled subunits that arise in the ER. To date, much of the analyses have focused on the involvement of HRD1/DER components in affecting the degradation of ERQC substrates. Although such components (Hrd1p/Der3p, Hrd3p, Der1p, Ubc7p, and Ubc1p) play a major role in the degradation of ERQC substrates such as CPY*, we have found that these substrates continue to be degraded at a significant rate in HRD1/DER-deficient cells. Fig. 1A shows the degradation kinetics of wild-type cells expressing CPY* compared with the congeneric strain lacking the HRD1-encoded ubiquitin ligase. As expected, the disruption of HRD1 significantly slowed the degradation rate of CPY* compared with that in wild-type cells, but instead of completely blocking CPY* degradation, a substantial rate of CPY* degradation still persists. Disruption of HRD3, DER1, or UBC7 gave similar results to that shown for the hrd1Δ strain (unpublished data). Double disruptions of HRD1/DER components (hrd1Δ der1Δ) did not further stabilize CPY* beyond that of the hrd1Δ disruption alone (Fig. 1A), confirming that these components are in the same pathway.

The finding that CPY* degradation continued in the absence of functional HRD1/DER components raised the possibility that the ERQC system possesses an additional mechanism or pathway with which to achieve the degradation of ERQC substrates. Previously, we found that anterograde vesicular transport from the ER to the Golgi apparatus was required for the efficient degradation of the lumenal ERQC substrates CPY* and PrA* (Caldwell et al., 2001). The degradative rate of CPY* and PrA* was reduced when either all vesicular transport from the ER was blocked through the use of the temperature-sensitive sec12–4 allele or when exit from the ER of specific cargo proteins such as CPY* and PrA* was impaired by the disruption of ERV29 (Caldwell et al., 2001). Given the strong possibility of an additional degradative mechanism/pathway, we undertook to determine if this ER-Golgi transport step was a component of the HRD1/DER pathway or of an independent pathway. Strains were constructed that were either lacking Hrd1p (hrd1Δ), blocked in ER-Golgi transport (erv29Δ or sec12–4), or both (hrd1Δ erv29Δ or...
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hrd1Δ and wild-type cells expressing single copy or overexpressed (OE) levels of CPY* (pAC453). (B) Wild-type (KHY163) and hrd1Δ (KHY171) strains expressing CPY* with and without overexpressed PrA*-HA (pAC540) present.

Figure 2. CPY* and PrA* can be degraded independently of the HRD/DER pathway. hrd1Δ and wild-type strains were radiolabeled, chased, and CPY* (A and B) immunoprecipitated at various times. Samples were analyzed as in Fig. 1. (A) Wild-type (KHY163) and hrd1Δ (KHY171) strains expressing single copy or overexpressed (OE) levels of CPY* (pAC453). (B) Wild-type (KHY163) and hrd1Δ (KHY171) strains expressing CPY* with and without overexpressed PrA*-HA (pAC540) present.

CPY* overexpression results in HRD/DER-independent degradation

In a separate project investigating the association between CPY* and the translocon in HRD/DER-deficient strains, CPY* was overexpressed approximately eightfold. Surprisingly, we observed that CPY* was now degraded with wild-type kinetics in a hrd1Δ strain instead of the expected slowed degradative rate (Fig. 2 A). The wild-type degradative rate caused by overexpression of CPY* was also observed in both der1Δ and hrd3Δ cells (unpublished data). This HRD/DER-independent degradation was further investigated using the ERQC substrate PrA*. PrA* was overexpressed in both wild-type and hrd1Δ strains, and the effect on the rate of single copy CPY* degradation was examined. Fig. 2 B shows that the overexpression of PrA*-HA also resulted in CPY* being degraded with wild-type kinetics in a hrd1Δ strain. This suggests that this HRD/DER-independent degradative mechanism is not specific for CPY* and capable of recognizing and degrading a variety of lumenal ERQC substrates.

Our working model is that the ERQC uses at least two distinct mechanisms to identify and degrade misfolded proteins from the ER: (1) the HRD/DER pathway using the components Hrd1p/Der3p, Hrd3p, Der1p, and Ubc7p; and (2) an alternative mechanism distinct from the HRD/DER pathway that we term the Hrd1p-independent proteolysis (HIP) pathway. Upon overexpression of ERQC substrates, the capacity of the HRD/DER pathway is likely saturated, and the remaining CPY* is accommodated by the alternative HIP mechanism. The two lines of evidence for a HRD/DER-independent alternative pathway are as follows: (1) the continuing degradation of ERQC substrates in HRD/DER-deficient strains that requires ER-Golgi transport; and (2) overexpression of ERQC substrates accelerates/restores the degradative rate in HRD/DER-deficient strains.
To confirm that a single mechanism is responsible for both of these observations, we formed several testable predictions that resulted from the integration of the ER-Golgi transport requirement and the HRD/DER pathway saturation model. First, in otherwise wild-type cells expressing single copy levels of CPY*, the absence of Erv29p should only moderately slow the degradative rate of CPY* as the HRD/DER pathway is functional. However, upon overexpression of CPY*, the HRD/DER components would be saturated and the vast majority of the CPY* would be diverted to the ER-Golgi transport–dependent pathway requiring Erv29p. Under these overexpression conditions, the disruption of ERV29, which impairs ER-Golgi transport, would now result in significantly enhanced stabilization of CPY*. Second, the high degree of CPY* stabilization in erv29Δ cells observed upon CPY* overexpression will be HRD/DER-independent, and therefore the disruption of HRD1 in such cells will have little additional stabilizing effect. Third, the stabilization of CPY* obtained by disabling both the HRD/DER components and ER-Golgi trafficking through a hrd1Δ erv29Δ double mutation should not be suppressed by overexpressing CPY*, as the alternative pathway has already been compromised by the disruption of ERV29. All three of these predictions were observed upon experimentation. Fig. 3A shows that the degradation of single copy levels of CPY* is slowed somewhat in an erv29Δ strain, and that the extent of stabilization was greatly increased upon overexpression of CPY*. As predicted, the imposition of a hrd1Δ mutation into the erv29Δ strain overexpressing CPY* does not further stabilize CPY* degradation (Fig. 3B). Finally, the very strong stabilization of CPY* observed in an erv29Δ hrd1Δ double mutant expressing single copy CPY* is not suppressed upon overexpression of CPY* (Fig. 3C).

In summary, overexpression of CPY* and PrA* appears to saturate the capacity of the HRD/DER pathway and quantitatively shifts such substrates to the alternative pathway requiring delivery to the Golgi apparatus. To confirm that CPY* does itself transit to the Golgi apparatus, we performed sequential immunoprecipitations on radiolabeled hrd1Δ cells overexpressing CPY*, first with anti-CPY antibodies, and then with anti–α1,6-mannose antibodies. Fig. 3D shows clearly that CPY* does indeed receive α1,6 mannose addition, which is indicative of delivery to the Golgi apparatus and confirms that this step is a requirement of HIP. Such a transport requirement for efficient degradation of overexpressed ERQC substrates might simply reflect that such substrates reach the Golgi apparatus, are subsequently secreted from the cell, and give the appearance of accelerated degradation or are alternatively sorted to the vacuole (lysosome equivalent) for degradation. Growth media was collected from radiolabeled wild-type (KHY171) cells overexpressing CPY* and erv29Δ (KHY270), hrd1Δ (KHY171), erv29Δ hrd1Δ (KHY279), and wild-type (KHY163) cells were analyzed as in Fig. 1. (A) erv29Δ and wild-type strains expressing either single copy or overexpressed (OE) levels of CPY* (pAC453). (B) Wild-type, hrd1Δ, erv29Δ, and hrd1Δ erv29Δ strains overexpressing (OE) CPY*. (C) Wild-type, hrd1Δ, and hrd1Δ erv29Δ strains either expressing single copy or overexpressed levels of CPY*. (D) hrd1Δ (KHY171) cells overexpressing CPY* were radiolabeled and CPY* immunoprecipitated. The precipitates were reimmunoprecipitated with either CPY* or α1,6-mannose antibodies.

Figure 3. The inhibition of ER-Golgi transport (erv29Δ) but not the HRD/DER pathway (hrd1Δ) significantly slows the degradation of overexpressed (OE) CPY*. erv29Δ (KHY270), hrd1Δ (KHY171), hrd1Δ erv29Δ (KHY279), and wild-type (KHY163) cells were analyzed as in Fig. 1. (A) erv29Δ and wild-type strains expressing either single copy or overexpressed (OE) levels of CPY* (pAC453). (B) Wild-type, hrd1Δ, erv29Δ, and hrd1Δ erv29Δ strains overexpressing (OE) CPY*. (C) Wild-type, hrd1Δ, and hrd1Δ erv29Δ strains either expressing single copy or overexpressed levels of CPY*. (D) hrd1Δ (KHY171) cells overexpressing CPY* were radiolabeled and CPY* immunoprecipitated. The precipitates were reimmunoprecipitated with either CPY* or α1,6-mannose antibodies.

Novick, 1987), which had no stabilizing effect on overexpressed CPY* degradation (unpublished data). The potential role of the vacuole was investigated by disrupting PEP4 in a hrd1Δ strain and determining the degradation rate of CPY* expressed at both single copy and overexpressed levels. The proteolytic activity of the vacuole is controlled by the PEP4-encoded PrA that, when disrupted, results in the vacuole lack-
We also investigated the degradation of CPY* in Samples were visualized by fluorography. or CPY was immunoprecipitated from intracellular (I) and extracellular (AACY9) cells expressing CPY were radiolabeled, chased, and CPY* hrd1 overexpressed levels of CPY* (pAC519). (B) wild-type (KHY163) cells overexpressing (OE) CPY* and hrd1 (KHY171) and wild-type (KHY163) cells overexpressing (OE) CPY* and vps10Δ (AAC91) cells expressing CPY were radiolabeled, chased, and CPY* or CPY was immunoprecipitated from intracellular (I) and extracellular (E) fractions as described previously (Cooper and Stevens, 1996). Samples were visualized by fluorography.

ing proteolytic activity and consequential stabilization of substrates degraded there (Jones et al., 1982). Fig. 4 A shows that rendering the vacuole proteolytically inactive has no stabilizing effect on CPY* when expressed at either normal or elevated levels. This result also eliminates a role for autophagy in HIP, as autophagocytosed substrates are degraded in the vacuole in a PEP4-dependent manner (Baba et al., 1997). We also investigated the degradation of CPY* in vps10Δ cells. Vps10p, the CPY sorting receptor, is also capable of sorting misfolded proteins from the trans-Golgi compartment to the vacuole (Hong et al., 1996). However, vps10Δ cells failed to stabilize overexpressed CPY* (unpublished data) and further indicated that the alternative degradation mechanism is not degrading substrates via delivery to the vacuole.

The HIP pathway involves the proteasome and ubiquitination

Cells deficient in the HRD/DER pathway remain capable of degrading overexpressed intracellular CPY* independently of the vacuole, which suggests that the other major intracellular proteolytic activity provided by the 26S proteasome would be responsible. Strains containing pre1 pre2 mutations are deficient in 26S proteasome activity and have been previously characterized to impair CPY* turnover (Hiller et al., 1996). If overexpression of CPY* diverts it to the alternative pathway, then a strain deficient in this pathway should not be capable of accelerating/restoring the CPY* degradation upon CPY* overexpression. Fig. 5 shows wild-type and congenic pre1 pre2 cells expressing either single copy or overexpressed CPY*. As expected, the degradation rate of single copy levels of CPY* is slowed considerably in the proteasome-compromised strain, but overexpression of CPY* fails to accelerate the turnover of CPY* in the pre1 pre2 strain and demonstrates that the proteasome is responsible for degrading overexpressed CPY*.

Both the HIP and HRD/DER pathways deliver ERQC substrates to the proteasome. The HRD/DER pathway achieves this by exporting CPY* through the translocon followed by Hrd1p-dependent ubiquitination (Plemper et al., 1997; Bays et al., 2001), but how is overexpressed CPY* delivered to the proteasome, and does it also involve ubiquitination? If HIP involves ubiquitination of overexpressed CPY*, then ubiquitinated forms of CPY* should be detectable in a hrd1Δ strain. This was tested by sequential immunoprecipitations of radio-labeled cells, first with anti-CPY antibodies followed by anti-ubiquitin-HA antibodies. Fig. 6 A (lanes 1–3) shows that CPY* in wild-type cells is heavily ubiquitinated, whereas ubiquitinated species of CPY* still existed in the hrd1Δ strain, albeit to a lesser extent. This HRD1-independent ubiquitin signal detected was specific to CPY*, as no ubiquitin signal was observed in a strain that lacked CPY* (pre1Δ).

Rsp5p is the ubiquitin ligase of the HIP pathway

The detection of ubiquitinated CPY* in a hrd1Δ strain requires that an additional E3 ubiquitin ligase participates in ERQC. We screened strains deficient in known or potential E3 enzymes, including the ER-localized DOA10 (Swanson et al., 2001), for impaired turnover rates of overexpressed CPY*. Ubiquitin ligases have either a RING-H2 motif or a HECT domain (Jackson et al., 2000), and using a PSI-BLAST homology search (Altschul et al., 1997), 31 proteins with significant homology to the RING-H2 domains of Hrd1p and Hrt1p were identified, whereas the 5 yeast proteins with HECT domains were previously known (Hochstrasser, 1996). The degradative rate of overexpressed CPY* was determined in the corresponding disruption or temperature-sensitive strains. Of the 36 potential ubiquitin ligases screened, only the essential gene RSP5 was necessary for the degradation of overexpressed CPY*. Fig. 6 B shows that degradation of overexpressed CPY* was significantly slowed in rps5Δ cells at the restrictive temperature. If RSP5 represents the ubiquitin ligase of the alternative pathway, then inactivating both Rsp5p and Hrd1p should completely stabilize single copy CPY* as both the alternative and HRD/DER pathways would be incapacitated. This was indeed the case as single copy CPY* is almost completely stable in a hrd1Δ rps5Δ strain (Fig. 6 C). Direct evidence that Rsp5p ubiquiti-nates ERQC substrates was that the ubiquitinated CPY* re-
remaining in a hrd1Δ strain is not observed in the rsp5–2 hrd1Δ double mutant (Fig. 6 A, lanes 3–5).

To confirm that Rsp5p is a component of the HIP pathway instead of a potential third degradative pathway, we introduced the rsp5–2 mutation into a strain deficient for the HIP pathway (erv29Δ). The stabilization of CPY* in an erv29Δ rsp5–2 double mutant was found to be no greater than either of the single mutants, indicating that Rsp5p is indeed a component of the HIP pathway (unpublished data). Furthermore, overexpression of CPY* in a hrd1Δ rsp5–2 strain does not suppress stabilization of CPY* (unpublished data).

The RING-H2 ubiquitin ligase Hrd1p has been demonstrated to use the ubiquitin-conjugating enzymes Ubc7p and Ubc1p (Friedlander et al., 2000; Bays et al., 2001) in the HRD/DER pathway. In contrast to Hrd1p, Rsp5p is a HECT domain ubiquitin ligase, and previous work has indicated that Rsp5p uses the ubiquitin-conjugating enzymes Ubc4p and Ubc5p (Gitan and Eide, 2000). If Ubc4p and Ubc5p act in concert with Rsp5p to mediate the degradation of ERQC substrates by the HIP pathway, then the absence of both Ubc4p and Ubc5p should impair the degradation of that substrate. The degradative rate of overexpressed CPY* was examined in both wild-type and ubc4Δ ubc5Δ cells, where it was found that the absence of Ubc4p and Ubc5p significantly slowed the degradation of CPY* (Fig. 6 D).

The HIP pathway is also capable of degrading integral membrane ERQC substrates

The finding that the ERQC possesses an alternative degradative pathway capable of degrading lumenal ERQC substrates raised the issue of whether integral membrane ERQC proteins such as Sec61–2p might also be an alternative pathway.

Figure 6. Rsp5p is the ubiquitin ligase of the HIP pathway and is responsible for the ubiquitination of CPY* in HRD/DER pathway-deficient cells. (A) Ubiquitination of CPY* in wild-type (lane 1), prc1Δ hrd1Δ (lane 2), hrd1Δ (lane 3), rsp5–2 (lane 4), and hrd1Δ rsp5–2 (lane 5) cells was assayed by radiolabeling at 37°C followed by sequential immunoprecipitations first with anti-CPY antibodies and then with anti–ubiquitin-HA antibodies. (B and C) rsp5–2 (KHY355), hrd1Δ (KHY171), hrd1Δ rsp5–2 (KHY359), and wild-type (KHY163) strains were radiolabeled, chased (at 37°C), and CPY* immunoprecipitated at various times. Samples were analyzed as in Fig. 1. (B) Wild-type and rsp5–2 cells overexpressing (OE) CPY* (pAC453). (C) Wild-type, hrd1Δ, rsp5–2, and hrd1Δ rsp5–2 expressing single copy levels of CPY*. (D) Wild-type (RH448) and ubc4Δ ubc5Δ (RH3097) overexpressing (OE) CPY*–HA were radiolabeled (at 30°C), chased, and CPY*–HA immunoprecipitated.

Figure 7. The integral membrane ERQC substrate Sec61–2p-HA can also be degraded by the HIP pathway. hrd1Δ (KHY171), rsp5–2 (KHY355), hrd1Δ rsp5–2 (KHY359), and wild-type (KHY163) cells were radiolabeled at 37°C (A) and 30°C (B), chased, Sec61–2p-HA immunoprecipitated at various times, and analyzed as in Fig. 1. (A) Wild-type, hrd1Δ, rsp5–2, and hrd1Δ rsp5–2 expressing Sec61–2p-HA (pAC460; Caldwell et al., 2001). (B) prc1Δ (KHY298) and prc1Δ hrd1Δ (KHY299) cells, in the absence of CPY*, expressing Sec61–2p-HA (pAC460) and wild-type (KHY163) and hrd1Δ (KHY171) in the presence of overexpressed (OE) CPY* expressing Sec61–2p-HA.
The ability of the alternative pathway to degrade Sec61–2p further stabilizes Sec61–2p. The findings that Sec61–2p is not fully stabilized (pAC453) of CPY* were analyzed as in Fig. 1. (KHY163) cells expressing single copy and overexpressed levels of Sec61–2p. Sec61–2p seems likely to be a substrate of an alternative pathway as, analogous to CPY* in Fig. 1 A, the disabling of the HRD/DER pathway reduced, but did not abolish, the degradation of Sec61–2p (Fig. 7 A). Wild-type cells, brd1Δ, rps5–2, or brd1Δ rps5–2 double mutants expressing Sec61–2p were radiolabeled at the restrictive temperature and the degradative kinetics of Sec61–2p were examined (Fig. 7 A). Even when the HRD/DER pathway is functional, Rsp5p contributes to the degradation of Sec61–2p as shown by the retarded degradative kinetics in the rps5–2 strain. Second, the inactivation of Rsp5p in cells lacking HRD/DER components (rps5–2 brd1Δ) further stabilized Sec61–2p. The findings that Sec61–2p is not fully stabilized in HRD/DER-deficient cells and that inactivation of the Rsp5p further stabilizes Sec61–2p suggest that integral membrane ERQC substrates can be degraded by the HIP pathway. The ability of the alternative pathway to degrade Sec61–2p was further demonstrated by overexpressing CPY* in brd1Δ cells also expressing Sec61–2p with the result that the retarded Sec61–2p degradation kinetics seen in brd1Δ cells was accelerated to those of a wild-type cell (Fig. 7 B).

The UPR regulates the HIP pathway

Of the many genes transcriptionally up-regulated by the UPR during ER stress (Travers et al., 2000), half have no known function attributed to them (Fewell et al., 2001). It is conceivable that components of the HIP pathway, like those of the HRD/DER pathway (Friedlander et al., 2000), may also be up-regulated during times of stress and therefore would be under UPR transcriptional control. If so, then disabling the UPR pathway would diminish or inactivate the HIP pathway. To test this possibility, CPY* was expressed either at single copy or overexpressed levels in wild-type cells or cells disrupted for IRE1. The absence of Ire1p had little significant effect on the degradation of single copy CPY* (Fig. 8), which is consistent with that previously reported (Friedlander et al., 2000), presumably because in the absence of the UPR the capacity of the HRD/DER pathway is sufficient to cope with single copy levels of CPY*. Overexpression of CPY* in an ire1Δ strain significantly slowed the turnover kinetics of CPY* (Fig. 8), which demonstrates that the HIP pathway requires a functional UPR.

Discussion

ERQC substrates continue to be degraded in the absence of a functional HRD/DER pathway using a newly identified alternative mechanism that requires ER-Golgi vesicular transport of substrates and the ubiquitin ligase Rsp5p before proteasomal degradation. This alternative system is distinct from the HRD/DER pathway, but together the two comprise the ERQC degradative capacity because only by disabling both pathways is degradation completely blocked. We propose the acronym HIP for the alternative mechanism. Overexpression of ERQC substrates appears to saturate the capacity of the HRD/DER pathway, resulting in the degradation of ERQC substrates to be completely dependent on the HIP pathway.

The ubiquitin ligase Rsp5p is a component of the HIP pathway and together with Hrd1p is responsible for the ubiquitination of CPY*. Only by inactivating both Rsp5p and Hrd1p does CPY* fail to be ubiquitinated and remains completely stable. Rsp5p-dependent ubiquitination involves the ubiquitin-conjugating enzymes Ubc4p and Ubc5p (Gitan and Eide, 2000), and these enzymes were also required by the HIP pathway to degrade overexpressed CPY*. In addition to its role in ERQC, Rsp5p is responsible for mediating ubiquitin-dependent protein sorting and trafficking within the secretory pathway. The ubiquitination of plasma membrane proteins by Rsp5p results in their internalization and subsequent transport to the vacuole for degradation (Galan et al., 1996; Hicke and Riezman, 1996). Rsp5p, acting in concert with Bul1p and Bul2p, can also ubiquitinate proteins such as Gap1p to direct them from the trans-Golgi compartment to the vacuole for degradation (Helliwell et al., 2001). However, the role of Rsp5p in ERQC is distinct from that involving vacuolar sorting, as the HIP pathway is independent of vacuolar proteases and instead utilizes the proteasome. Furthermore, the disruption of both BUL1 and BUL2 has no effect on the degradation rate of CPY* (unpublished data).

Examination of the mechanisms used by mammalian cells to degrade ERQC substrates suggests extensive overlap with the HIP pathway described here. This similarity includes the observation of the following ERQC substrates in post-ER compartments (ER-Golgi intermediate compartment and/or Golgi subcompartments): unassembled MHC class I molecules (Hsu et al., 1991), misfolded G protein of vesicular stomatitis virus (Hammond and Helenius, 1994), mutant forms of sucrase-isomaltase and lysosomal α-glucosidase (Moolenaar et al., 1997), and precursors of human asialoglycoprotein receptor H2a (Kamhi-Nesher et al., 2001). The soluble secretory form of IgM molecules in differentiated B lymphocytes is degraded intracellularly in a manner completely dependent on transport to a post-ER compartment (Winitz et al., 1996), and truncated versions of CFTR reach the Golgi apparatus before degradation by the proteasome (Benharouga et al., 2001). Further evidence suggesting the involvement of post-

Figure 8. The UPR is required for efficient degradation of overexpressed (OE) CPY*. ire1Δ (KHY280) and wild-type (KHY163) cells expressing single copy and overexpressed levels (pAC453) of CPY* were analyzed as in Fig. 1.
ER compartment(s) is that some ERQC components are themselves found in post-ER locations: UDP-glucose:glycoprotein glucosyltransferase (UGGT), an important ERQC glycoprotein folding sensor, is found in post-ER vesicles (Zuber et al., 2001), whereas endoplasmic-reticulum α-mannosidase has been implicated in quality control and was localized to the cis/medial-Golgi apparatus (Zuber et al., 2000).

How far through the secretory pathway do ERQC substrates such as CPY* progress and what function would delivery of ERQC substrates to the Golgi apparatus serve? CPY* in either DER1-deficient cells (Knop et al., 1996) or those lacking an ER-localized proposed ERQC lectin (mnl1Δ/htm1Δ) (Jakob et al., 2001; Nakatsukasa et al., 2001) received α1,6-mannose addition but not α1,3-mannose addition, indicating that CPY* reached the cis-Golgi but not the trans-Golgi compartment (Brisgog et al., 2000). Similarly, we have also found that CPY* is delivered to the cis-Golgi compartment when overexpressed in hrd1Δ cells as evidenced by the addition of α1,6-mannose. A recent report has shown that a heterologously expressed fusion ERQC substrate Kar2 hemagglutinin neuraminidase receives O-linked glycosylation indicative of it reaching the yeast cis/medial-Golgi apparatus, whereas both KHN and CPY* can be found in vitro ER-derived COPII vesicles (Vashist et al., 2001). Vashist et al. (2001) concluded that all the KHN is delivered to the Golgi apparatus, and then is returned to the ER where it is exported to the cytosol and likely ubiquitinated by Hrd1p. However, we suggest another possibility wherein KHN (much like CPY*) is degraded via two distinct pathways (HIP and HRD1/DER), in which a portion of KHN is retained in the ER and is exported and ubiquitinated by Hrd1p while the remaining KHN is transported to the Golgi apparatus and eventually ubiquitinated by Rsp5p.

After transportation to the Golgi apparatus, CPY* must then be exported from within the secretory pathway to the cytosol to be accessible to the cytosolically located Rsp5p. Therefore CPY* is likely returned from the Golgi apparatus to the ER where it is exported to the cytosol, presumably through the translocon, and subsequently ubiquitinated by Rsp5p before proteasomal degradation. A highly speculative alternative model involves the export of CPY* directly from the cis-Golgi compartment to the cytosol by an unidentified mechanism before ubiquitination by Rsp5p. These two possibilities are presented in the model shown in Fig. 9. Unfortunately, the broad subcellular distribution of Rsp5p provides no indication as to which model is correct (Gajewska et al., 2001). Rsp5p can presumably associate with both the Golgi apparatus to mediate Gap1p sorting (Helliwell et al., 2001) and the ER, as evidenced by its ubiquitination of the nuclear membrane/ER-restrained transcription factor Spt23p (Hoppe et al., 2000). Although ERQC substrates are likely returned to the ER from the Golgi apparatus, such a requirement has yet to be definitively demonstrated. The use of Golgi to ER retrograde trafficking mutants is problematic as those mutants tested also show defects in forward transport over the time course required for the degradation experiments (unpublished data). The rationale for delivering ERQC substrates to the Golgi apparatus may be either to (a) access a mechanism responsible for exporting it directly from the Golgi apparatus to the cytosol, or (b) to receive a Golgi apparatus-based modification that signals either its efficient translocation to the cytosol or its return to the ER or its efficient ubiquitination by Rsp5p on its retrotranslocation from the ER to the cytosol. We favor an alternative model in which ERQC substrates are not actively targeted to the Golgi apparatus, but instead are inadequately retained in the ER due to saturation of this pathway. Therefore the cis-Golgi apparatus may act as a quality control catchment system to capture ERQC substrates that have “escaped” the ER before returning them by retrograde transport to the ER.
others (Friedlander et al., 2000) to explain either the continued degradation of ERQC substrates in *HRD1/DER*-deficient cells or the surprising finding that cells deficient for the *HRD1/DER* pathway display no growth defects even when expressing misfolded proteins in the ER. However, double mutants lacking both the UPR and *HRD1/DER* pathways display significantly impaired growth phenotypes that are further exacerbated by ER stress (Friedlander et al., 2000; unpublished data). These observations are consistent with our findings that the HIP pathway is likely under UPR control such that the *hrd1Δ ire1Δ* mutant is deprived of both of its options in dealing with ER stress. Consistent with this model of UPR-regulated HIP, the identification of a number of genes under UPR transcriptional regulation that are involved in ER to Golgi vesicular transport and therefore likely necessary for the HIP pathway (Travers et al., 2000).

The importance of preventing both the aggregation of misfolded proteins in the ER and the transport of these proteins to the cell surface is underscored by the fact that the cell uses at least two distinct mechanisms to effect their degradation. However, this apparent redundancy raises the question of why one would observe any stabilization of ERQC substrates in *HRD1/DER*-deficient cells while the HIP pathway is functional. It is possible that the two systems complement each other, with the *HRD1/DER* pathway comprising a low capacity system for contendling with the nominal loads of misfolded proteins accruing in the ER under optimal growth conditions. The HIP pathway might act as a high capacity system that is up-regulated, potentially by the UPR, to accommodate increased levels of ERQC substrates.

In summary, we have identified an *HRD1/DER*-independent degradation mechanism in which ER-Golgi trafficking and Rsp5p-dependent ubiquitination is required before degradation by the proteasome. Further work will identify the purpose of delivering ERQC substrates to the Golgi apparatus, where in the cell ERQC substrate ubiquitination by Rsp5p occurs, and how such substrates gain access to the Rsp5p in the cytosol.

### Materials and methods

#### Plasmids, media, and strain construction

Media were prepared as described previously (Hill and Stevens, 1994). To introduce *prc1Δ::KAN, ubc7Δ::KAN, ire1Δ::KAN*, and *hrd1Δ::KAN* alleles into strains, oligonucleotides flanking the disrupted allele were used to amplify the allele from strains of the *S. cerevisiae* Genome Deletion Project (Research Genetics). The product was then transformed into a strain with subsequent selection on YEPD media containing 200 μg/ml G418. Disruptions were confirmed by PCR analysis on genomic DNA using oligonucleotides flanking each disrupted locus. WCG4a and WCG1-1121a (provided by Dieter Wolf, Universitad Stuttgart, Stuttgart, Germany) were transformed with the *prc1Δ::KAN* allele to make strains KYH292 and KYH293; *ire1Δ::KAN* was transformed into KYH163 to create KYH280; *ubc7Δ::KAN* was transformed into KYH163 to make KYH313; and *hrd1Δ::KAN* was transformed into KYH355 to create KYH359.

KYH163 was constructed as described previously (Caldwell et al., 2001). KYH171 was created by replacing the vma22Δ locus of KYH140 (Hill and Cooper, 2000). The *prc1Δ::KAN* allele was amplified by PCR and inserted into pTOPO 2.1 (Invitrogen) to create pAC550. A 0.9-kb ClaI-SalI fragment from pAC550 was replaced with the *HIS3*-containing Clal-SalI fragment from pJL217 to create pAC556. The *hrd1Δ::HIS3* allele from pAC556 was amplified by and transformed into KYH163 and KYH171, creating strains KYH298 and KYH299, respectively. The disruption was confirmed by PCR and Western blot (Caldwell et al., 2001). The *pep4Δ::TRP1* allele from Sacr-Xhol-digested pSL1-10 (provided by Dr. Steven Nothwehr, University of Missouri, Columbia, MO) was introduced into KYH171 to create KYH265. The *ubc7Δ::HIS3* allele was amplified by from RH3140 (provided by Dr. Linda Hicke, Northwestern University, Evanston, IL), and transformed into KYH313, creating KYH333.

The *hrd1Δ::TRP1* allele was constructed by inserting a TRP1-containing BglII fragment from pJL248 into BglII-NsiI-digested pAC370 (Hill and Cooper, 2000) creating pAC401. The *hrd1Δ::TRP1* allele from Drai-digested pAC401 was introduced into KYH127 (Hill and Cooper, 2000) and KYH270 (Caldwell et al., 2001) to create strains KYH158 and KYH279, respectively. KYH237 was created by replacing the vma22Δ locus in KYH158.

To introduce the sec12–4 allele and create KYH306 and KYH308, SalI-digested pAC559, was transformed into KYH163 and KYH171, and Ura prototrophs were placed on S-FOA. Ura colonies were screened by fail-to grow at 38°C. pAC559 was created by ligating a sec12–4 containing 3.4-kb Xhol-XbaI from pSH2–1 (provided by Dr. Akihiko Nakano, RIKEN, Wako, Saitama, Japan) into Xhol-Spel-digested pSK306. The *rps5–2* allele was introduced by transforming KYH163 with Sul-digested pKM017 (provided by Dr. Stefan Jentsch, Max Plank Institute of Biochemistry, Martinsried, Germany). Rsp5 was then deleted by transforming the *hrd1Δ::HIS3*-containing fragment from Sacr-Sphl-digested pKM017.

Strains deleted for potential ubiquitin ligase genes were transformed with pAC578, radiolabeled, and CPY–HA was immunoprecipitated at various times (Hill and Cooper, 2000). Potential RING-H2–containing proteins were as follows: YFL010C, YHR075C-A, YKL034C, YLR214C, YOR118C, YOR191W, YOR207W, YLR427W, YMR247C, YOR143C, YLR302W, YPR093C, YNL116W, YBR114W, YLR148W, YER068W, YIL030C (DOA10/SSM4), YER116C, YDL074C, YBR062C, and YDL013W, and strains deleted/temperature sensitive allele for HECT domain–containing proteins are YJR036C, YDR457W, YKL010C, YG2141W, and YER125W.

pAC453 and pAC19 are 2-μm plasmids and pAC446 is a CEN plasmid in which a *prc1Δ::CEN* containing 2.8-kb SacI-Sall fragment was created from pAC536 (Hill and Cooper, 2000) was ligated into the SacI-Sall sites of pTV3,YEp352, and pRS315, respectively. pAC578 was created by ligating a CPY–3XHA–containing 4.3-kb SacI-Xhol fragment from pB15 (provided by Dr. Scott Moye-Riley, University of Iowa, Iowa City, IO) into SacI-BamHI–digested YEp352. pAC540 is a 2-μm plasmid in which the 1.9-kb SacI-BglII fragment containing *CEN*–HA from pAC355 (Caldwell et al., 2001) was ligated in SacI-BamHI–digested YEp352.

Radiolabeling, immunoprecipitation, and antibodies

Radiolabeling and immunoprecipitation were performed as described previously (Hill and Cooper, 2000; submitted to J. Biol. Chem.). The gels were fixed, dried, and exposed either to a phosphor cassette (Molecular Dynamics) or to X-ray film. Quantification of gels was performed as described previously (Hill and Cooper, 2000).

### References


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